

Cry-5719

GenCore version 5.1.9  
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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 23:54:16 ; Search time 41.28 Seconds  
(without alignments)  
4222.534 Million cell updates/sec

Title: US-10-750-622-5719  
Perfect score: 25  
Sequence: 1 aacacactgggacatgctcgattc 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_8:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*  
15: geneseqn2006s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

| Result<br>No. | Score | Query<br>Match | Length | DB | ID       | Description        |
|---------------|-------|----------------|--------|----|----------|--------------------|
| 1             | 19.2  | 76.8           | 4141   | 10 | ADE57243 | Ade57243 Rat gene  |
| 2             | 17.8  | 71.2           | 1524   | 2  | AAV32819 | Aav32819 Human dea |

rn1-S19

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 19:04:00 ; Search time 10.76 Seconds  
(without alignments)  
4347.372 Million cell updates/sec

Title: US-10-750-622-5719

Perfect score: 25

Sequence: 1 aacacactgggacatgctcgattc 25

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result | No. | Score | Query |        |    |                      | Description       |
|--------|-----|-------|-------|--------|----|----------------------|-------------------|
|        |     |       | Match | Length | DB | ID                   |                   |
| c      | 1   | 17.8  | 71.2  | 601    | 3  | US-09-949-016-28895  | Sequence 28895, A |
| c      | 2   | 17.8  | 71.2  | 601    | 3  | US-09-949-016-140881 | Sequence 140881,  |
|        | 3   | 17.8  | 71.2  | 37622  | 3  | US-09-949-016-12294  | Sequence 12294, A |
|        | 4   | 17.8  | 71.2  | 37622  | 3  | US-09-949-016-15726  | Sequence 15726, A |
|        | 5   | 17.8  | 71.2  | 767677 | 3  | US-09-949-016-12147  | Sequence 12147, A |
|        | 6   | 17.8  | 71.2  | 767677 | 3  | US-09-949-016-17361  | Sequence 17361, A |
|        | 7   | 17.6  | 70.4  | 709    | 3  | US-09-270-767-7641   | Sequence 7641, Ap |

rng-4518

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 23:54:16 ; Search time 990.72 Seconds  
(without alignments)  
4222.534 Million cell updates/sec

Title: US-10-750-622-4518

Perfect score: 599.6

Sequence: 1 aaattttcttcctcctct.....cgcagcattaaaagagggcc 600

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5244920 seqs, 3486124231 residues

Total number of hits satisfying chosen parameters: 10489840

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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10: geneseqn2003cs:  
11: geneseqn2003ds:  
12: geneseqn2004as:  
13: geneseqn2004bs:  
14: geneseqn2005s:  
15: geneseqn2006s:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

%

| Result<br>No. | Score | Query |        |    |            | Description        |
|---------------|-------|-------|--------|----|------------|--------------------|
|               |       | Match | Length | DB | ID         |                    |
| 1             | 50.8  | 8.5   | 59446  | 10 | AAD47904   | Aad47904 Human tra |
| 2             | 50.4  | 8.4   | 110000 | 14 | AEE04876_1 | Continuation (2 of |

rni-4518

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OM nucleic - nucleic search, using sw model

Run on: January 21, 2007, 19:04:00 ; Search time 258.24 Seconds  
(without alignments)  
4347.372 Million cell updates/sec

Title: US-10-750-622-4518  
Perfect score: 599.6  
Sequence: 1 aaattttcttcctcctct.....cgcagcattaaaagaggccc 600

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1403666 seqs, 935554401 residues

Total number of hits satisfying chosen parameters: 2807332

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /EMC\_Celerra\_SIDS3/ptodata/2/ina/1\_COMB.seq:\*

2: /EMC\_Celerra\_SIDS3/ptodata/2/ina/5\_COMB.seq:\*

3: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6A\_COMB.seq:\*

4: /EMC\_Celerra\_SIDS3/ptodata/2/ina/6B\_COMB.seq:\*

5: /EMC\_Celerra\_SIDS3/ptodata/2/ina/7\_COMB.seq:\*

6: /EMC\_Celerra\_SIDS3/ptodata/2/ina/H\_COMB.seq:\*

7: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PCTUS\_COMB.seq:\*

8: /EMC\_Celerra\_SIDS3/ptodata/2/ina/PP\_COMB.seq:\*

9: /EMC\_Celerra\_SIDS3/ptodata/2/ina/RE\_COMB.seq:\*

10: /EMC\_Celerra\_SIDS3/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result | Query |       |        |        |                     | Description       |
|--------|-------|-------|--------|--------|---------------------|-------------------|
|        | No.   | Score | Match  | Length | DB                  |                   |
| ID     |       |       |        |        |                     |                   |
| c 1    | 52.4  | 8.7   | 55841  | 3      | US-09-949-016-16602 | Sequence 16602, A |
| c 2    | 50.8  | 8.5   | 601    | 3      | US-09-949-016-70771 | Sequence 70771, A |
| c 3    | 50.8  | 8.5   | 61462  | 3      | US-09-949-016-17522 | Sequence 17522, A |
| c 4    | 49.6  | 8.3   | 106924 | 3      | US-09-949-016-13834 | Sequence 13834, A |
| c 5    | 46.6  | 7.8   | 300402 | 3      | US-09-949-016-13632 | Sequence 13632, A |
| c 6    | 45.2  | 7.5   | 670689 | 3      | US-09-949-016-12505 | Sequence 12505, A |
| c 7    | 45.2  | 7.5   | 670690 | 3      | US-09-949-016-14207 | Sequence 14207, A |